MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR
PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF
AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA
LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE
GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH

Fig. 1

```
TCCGCAGGCGGACCGGGGGCAAAGGAGGTGGCATGTCGGTCAGGCACAGCAGGGTCCTGT
GTCCGCGCTGAGCCGCGCTCTCCCTGCTCCAGCAAGGACC
><Met (trans=1-s, dir=f, res=1)>
ATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTGTGCCTGGTGTTGGCGCTGCCTGCC
CTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTACCCCTGGCGGGAC
GCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGG
CCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG
TTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAG
GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTC
GCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCC
CCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCC
AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCC
CTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCC
CTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT
GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGG
CGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC
TGATCCTGGCCCCCTCTTATTTATTCTACATCCTTGGCACCCACTTGCACTGAAAGAGG
CTTTTTTTTAAATAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAAAAA
```

Fig. 2

```
GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGG
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
GAACACGCAGTGCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC
TCCAGCTCAGAGCAGTGCCAGCCCCACGCAACTGCACGGCCCTGGGCCT
GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
```

Fig . 3

SEQ ID No:4   128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGGCGGCCACTACACG
SEQ ID No:5   1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGGCGGCCACTACACG
SEQ ID No:6   1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGGCGNACTACACG
SEQ ID No:3   1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGGCGGCCACTACACG   G

SEQ ID No:4   178 CA-TTCTGGAACTACCTGGAGCGC
SEQ ID No:5   51 CAGTTCTGGAANTAACTGGAGCNCTGCCCGCTACTGNAACGTCCTCTGNGG
SEQ ID No:6   2 CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGG
SEQ ID No:3   51 CAGTTCTGGAANTAACTGGAGCNCTGCCCGCTACTGNAACGTCCTCTGNGG

SEQ ID No:5   101 GGAGCCNTGAGGAGGAGGCANGNGCTTGCCACGCACCACCAACGGCGCCT
SEQ ID No:6   52 GGAGCCGTGAGGAGGAGGCACGGGCTTGCCACGCACCACCAACCGTGCCT
SEQ ID No:7   1   GAGGGCCCCCAGGAGTGGTGGCCGGAGGTG
SEQ ID No:3   101 GGAGCCGTGAGGAGGAGGCACGGGCTTGCCACGCACCACCACCAACCGTGCCT

SEQ ID No:5   151 GCNGCTGCAGCACCGGNTTCTTCGGCACGCTGNTTTCTGCTTGGAGCAC
SEQ ID No:6   102 GCCGCTGCCGCACCGGCTTCTTCGGCACGCTTTCTGCTTGGAGCAC
SEQ ID No:7   32 TGGCAGGGGTCAGGTTGCTGGTCCCCAGCCTTGCACCCTGAGCTAGGACAC
SEQ ID No:3   151 GCCGCTGCCGCACCGGCTTCTTCGGCACGCTGGTTTCTGCTTGGAGCAC

SEQ ID No:5   201 GCATCGGTGTCCACCTGGTGNCGGCGGTGATTGCNCCGGGCACCCCCAGCCA
SEQ ID No:6   152 GCATCGGTGTCCACCTGGTGGCGGCGGTGATTNCCCGGGCACCCCCAGCCA
SEQ ID No:7   82 CAGTTCCCCTGACCCTGTTCTCCCTCCTGGCTGCAGGCACCCCCAGCCA
SEQ ID No:8   1 GCATCGGTGTCCACCTGGTGCCGGCGGTGATTGCCCGGGCACCCCCAGCCA
SEQ ID No:10   1   CTTGTCCACCTGGTGCCGGCGGTGATTNCCC-GGGCACCCCCAGCCA
SEQ ID No:3   201 GCATCGGTGTCCACCTGGTGCCGGCGGTGATTGCCCGGGCACCCCCAGCCA

Fig. 4

```
SEQ ID No:5   251  GAACACGCA-TGCAAAGCCGTG
SEQ ID No:7   132  GAACACGCAGN-CC-AGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID No:8    51  GAACACGCAG-GCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID No:10   47  GAACACGCAGTGCC-AGCCNT-CCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID No:9     1                      AGCNGTGCNCNCAGGCACCTTCTCAGCCAGCAGT
SEQ ID No:3   251  GAACACGCAGTGCCTAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGC

SEQ ID No:7   182  TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID No:8   101  TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID No:10   97  TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID No:9    36  TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCAAGCGCCCTGGNC-T
SEQ ID No:3   301  TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT

SEQ ID No:7   232  GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAG
SEQ ID No:8   151  GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
SEQ ID No:10  147  GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
SEQ ID No:9    86  GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCGCTGTGCACCAGCT
SEQ ID No:3   351  GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT

SEQ ID No:10  197  GCACTGGCTTCCCCCTCCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
SEQ ID No:9   136  GCACTGGCTTCCCCCTCCAGCACCAGGGTANCAGGAGCTGAGGAGTGTGAG
SEQ ID No:3   401  GCACTGGCTTCCCCCTCCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG

SEQ ID No:10  247  CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID No:9   186  CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID No:3   451  CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
```

Fig. 4. (CONT.)

DNA 30942
hTNFR2

DNA 30942
hTNFR2

DNA 30942
hTNFR2

DNA 30942
hTNFR2

DNA 30942
hTNFR2

DNA 30942
hTNFR2

DNA 30942
hTNFR2

hTNFR2

hTNFR2

hTNFR2

CRD 1

CRD 2

CRD 2

CRD 3

CRD 3

CRD 4

CRD 4

Fig. 5

```
DcR3   1  M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A   31
OPG    1  M N K L L C C A L V F L D I S I K W T T Q E T F P . . . . . .   25

                               ┌─────────────────── CRD1 ───────────────────
DcR3   32 E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C   62
OPG    26 . . P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C   54

          ────────────────────────────┐  ┌──────────────────────────────
DcR3   63 R R D S P T C G P C P P R H Y T Q F W N Y L E R C R Y C N V     93
OPG    55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P   85

          ───────────────────── CRD2 ─────────────────────────┐  ┌──────
DcR3   94 L C G E R E E E A R A C H A T H N R A C R C R T G F F A H A G   124
OPG    86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E   116

          ──────────────────────── CRD3 ──────────────────────────┐  ┌──
DcR3   125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P  155
OPG    117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D  147

          ────────────────────────── CRD4 ──────────────────────────
DcR3   156 G T F S A S S S S E Q C Q P H R N C T A L G L A L N V P G S   186
OPG    148 G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G N   178

          ────────────────────────┐
DcR3   187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D   217
OPG    179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R   208

DcR3   218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T . P R   247
OPG    209 F A V P T K F T P N W L S V L L V D N L P G T K V N A E S V E R   239

DcR3   248 A G R A A L Q L K L R R R L T E L L G A Q D G A L . L V R L L   277
OPG    240 I K R Q H S S Q E Q T F Q L L K L L W K H Q N K A Q D I V K K I  270

DcR3   278 Q A L R V A R M P G L E R S V R E R F L P V H 300
OPG    271 I Q D I D L C E N S V Q R H I G H A N L T F E 293 . . .
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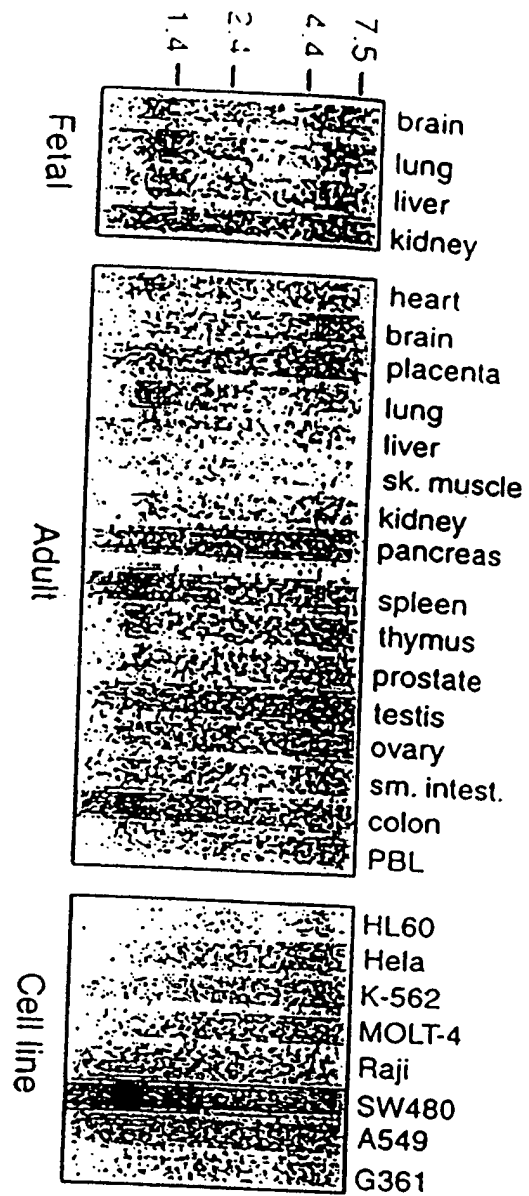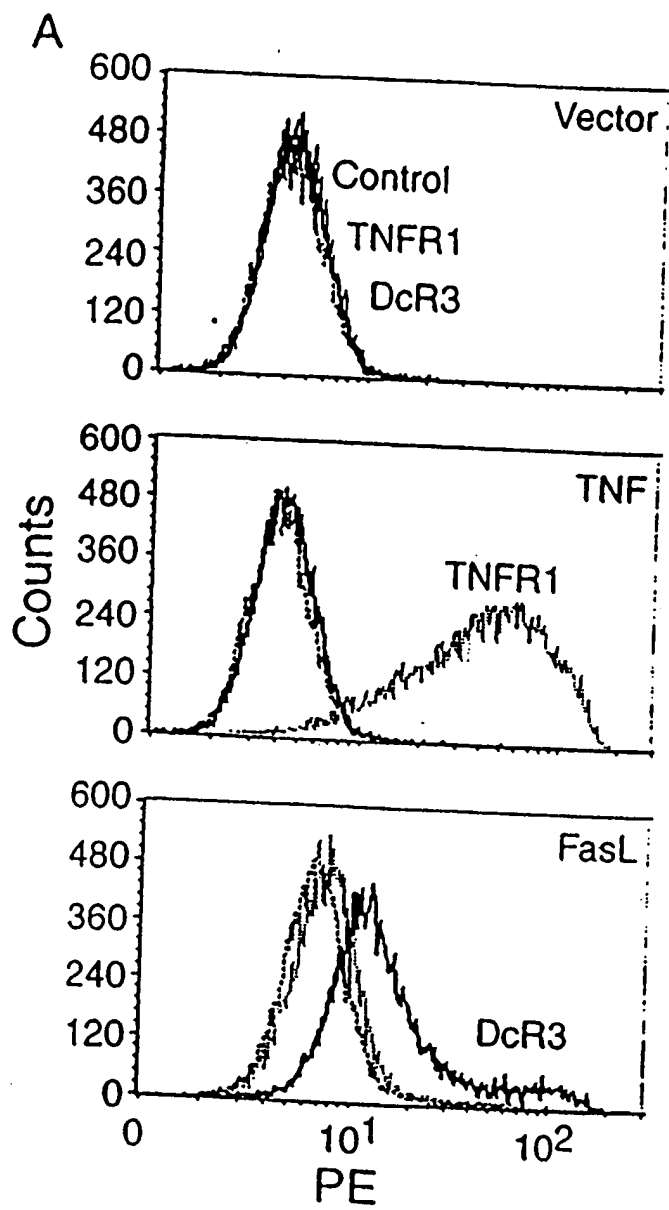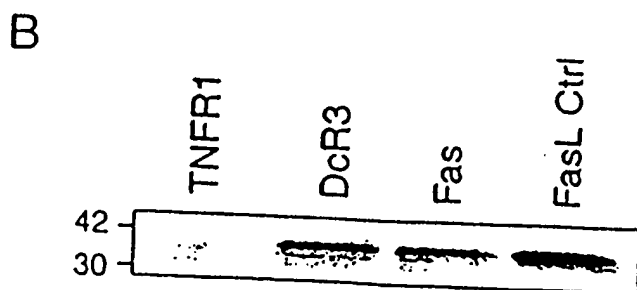
Fig. 6

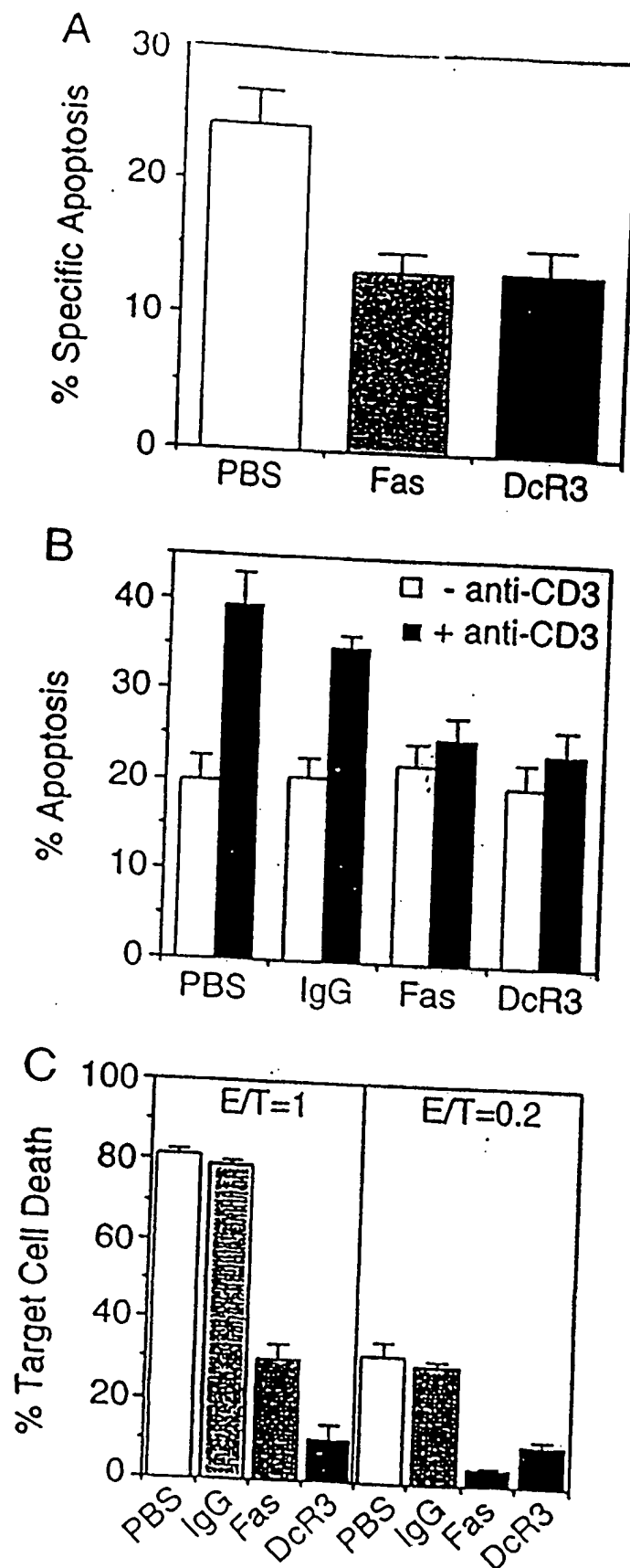Fetal

brain
lung
liver
kidney

Adult

heart
brain
placenta
lung
liver
sk. muscle
kidney
pancreas
spleen
thymus
prostate
testis
ovary
sm. intest.
colon
PBL

Cell line

HL60
Hela
K-562
MOLT-4
Raji
SW480
A549
G361

7.5
4.4
2.4
1.4

Fig. 7

Fig. 8

Fig. 9

Fig. 10

Human MLR

Fig. 11A

Murine MLR

Fig. 11B

Human Costimulation
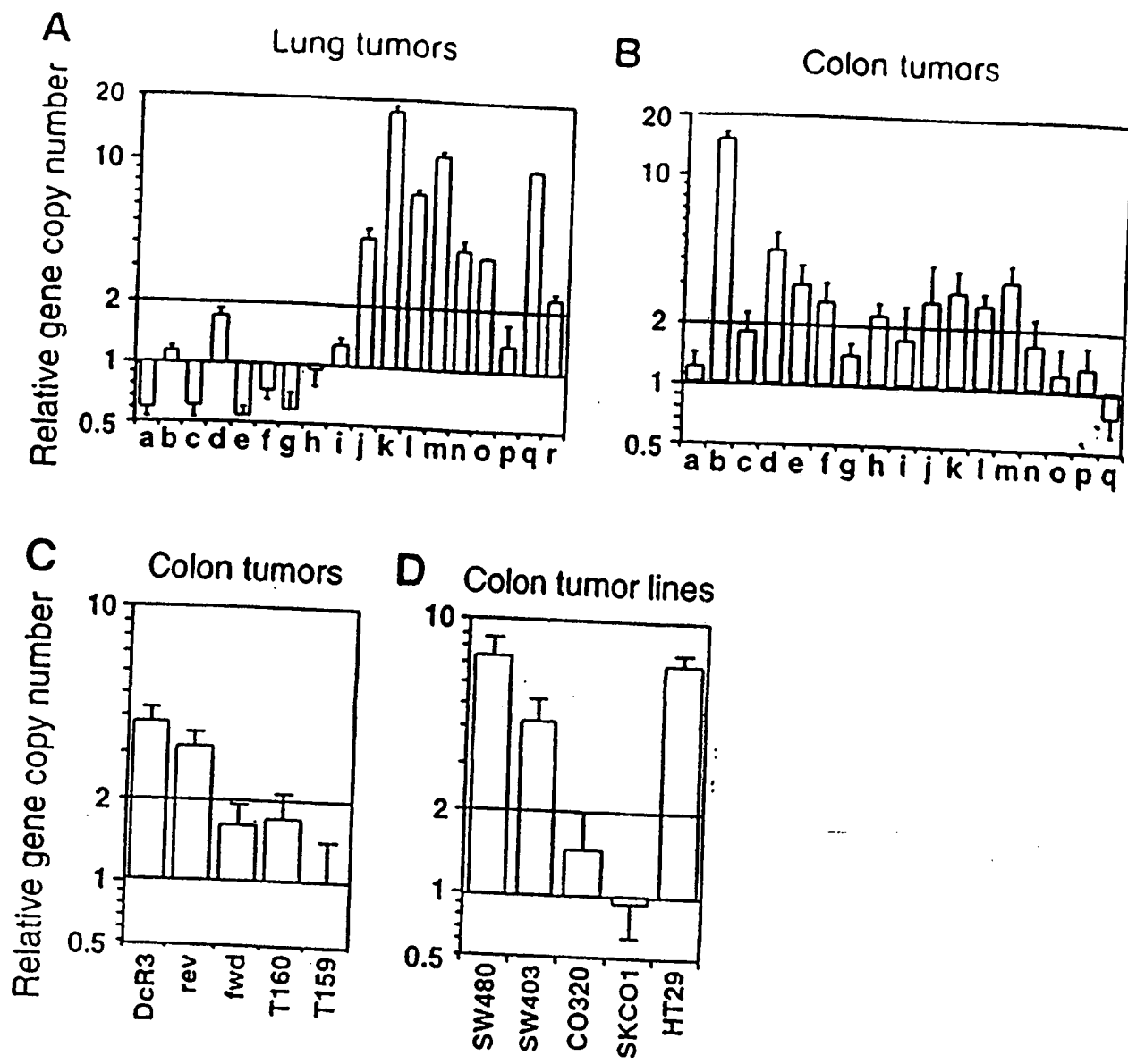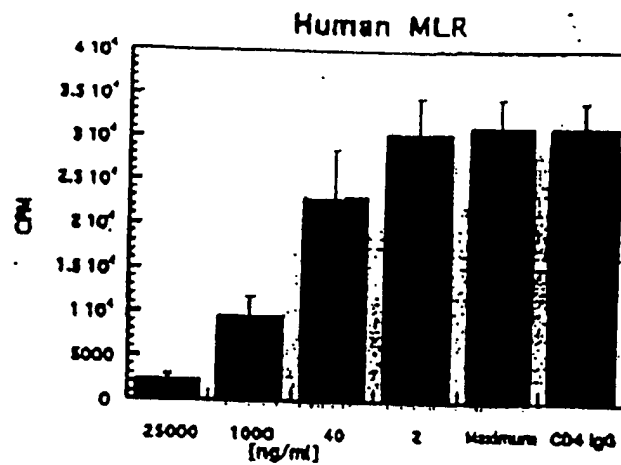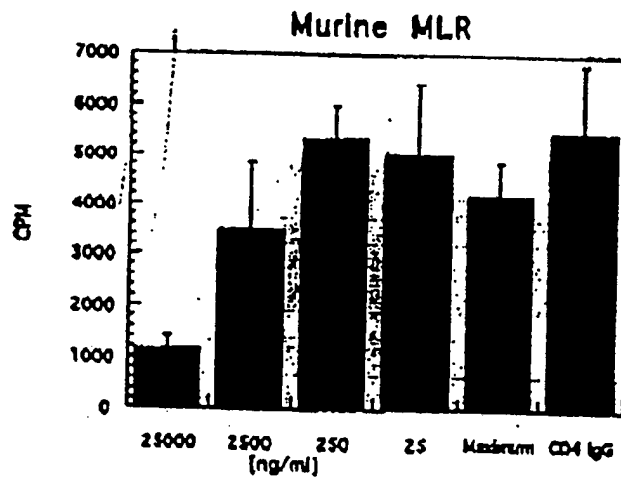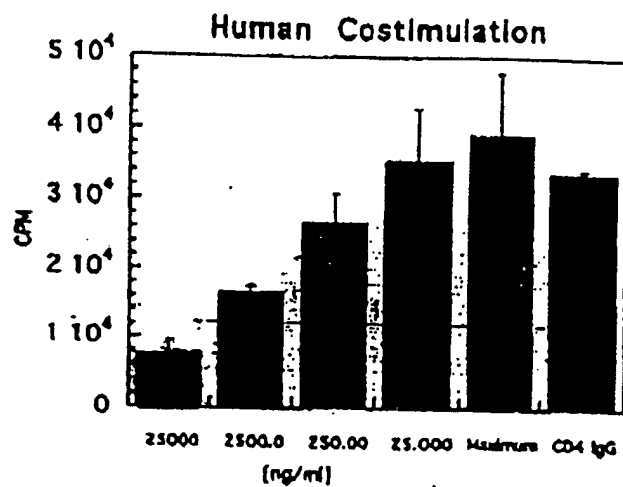
Fig. 11C

FIGURE 12

mAb	Isotype	Antigen Specificity (ELISA)					% Blocking (ELISA)
		DcR3	DR4	DR5	DcR1	OPG	
4B7.1.1	IgG1	+++	-	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	-	++
8D3.1.5	˙IgG1	+++	-	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.

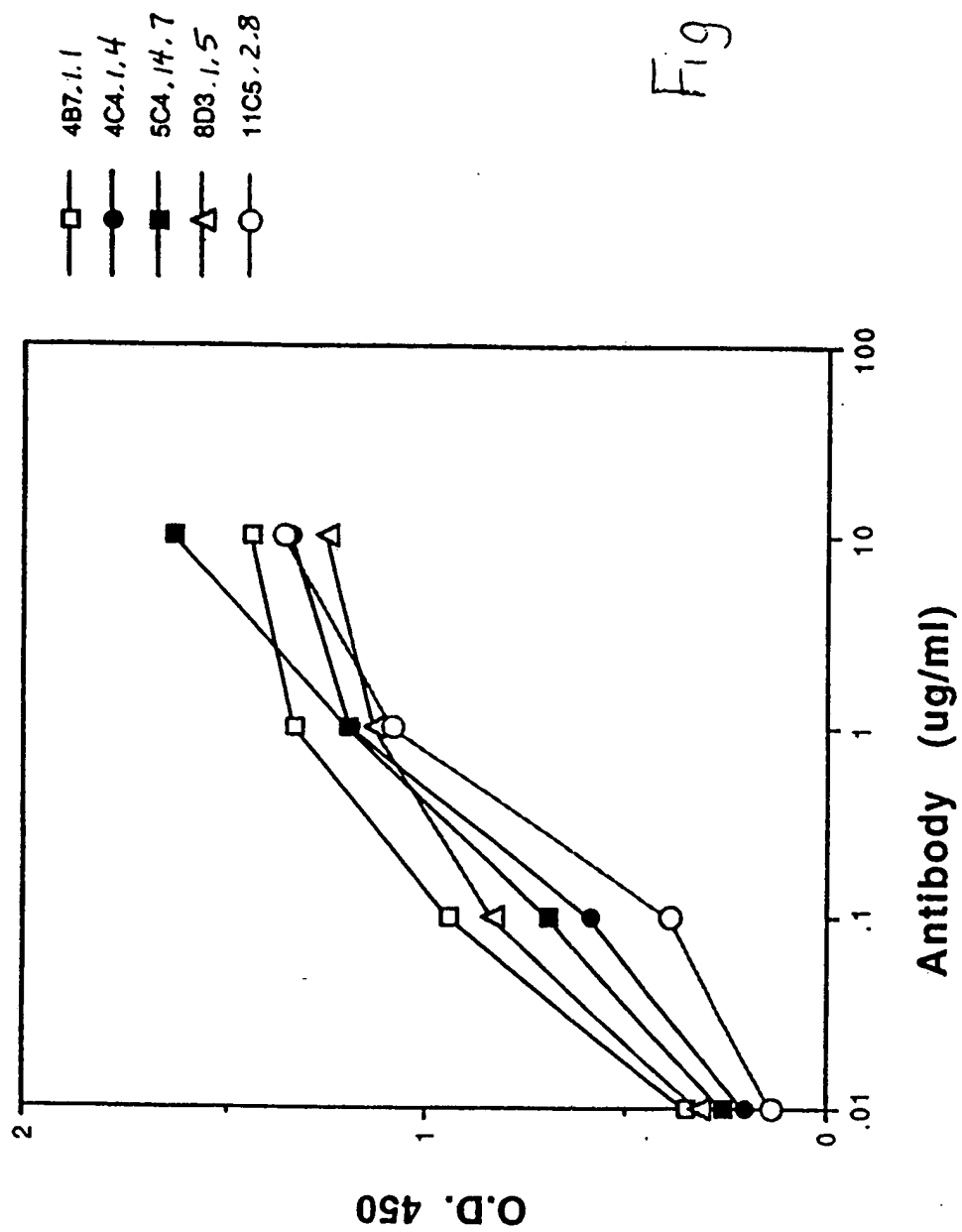% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

Fig. 13

4B7.1.1
4C4.1.4
5C4.14.7
8D3.1.5
11C5.2.8

O.D. 450

Antibody (ug/ml)

Fig. 14